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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: Tue Sep 18 13:40:24 EDT 2007

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Application No: 10644084 Version No: 3.0

Input Set:

Output Set:

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Finished: 2007-09-12 14:17:30.849
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 56 ms
Total Warnings: 4
Total Errors: 0
No. of SeqIDs Defined: 9
Actual SeqID Count: 9

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<150> JP 2002-284263

<151> 2002-09-27

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<170> PatentIn version 3.3

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<222> (80)..(1927)

<223> /note="afadin-and alpha-actinin-binding protein"

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Met Gly Asp Trp Met Thr Val Thr Asp Pro Val
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15 20 25atg tct ccg tcc agt ttg tac tcc cag caa gtt ctg tgc tct tca gta 208
Met Ser Pro Ser Ser Leu Tyr Ser Gln Gln Val Leu Cys Ser Ser Val
30 35 40cct tta tcc aaa aac gtg cat ggt gtt ttc ggt gtc ttc tgc aca gga 256
Pro Leu Ser Lys Asn Val His Gly Val Phe Gly Val Phe Cys Thr Gly
45 50 55gag aac att gaa caa agt att tcc tat ctt gat cag gag ctg acc acc 304
Glu Asn Ile Glu Gln Ser Ile Ser Tyr Leu Asp Gln Glu Leu Thr Thr
60 65 70 75ttc ggg ttt cct tcc ttg tat gaa gaa tcc aaa agt aaa gag gca aag 352
Phe Gly Phe Pro Ser Leu Tyr Glu Ser Lys Ser Lys Glu Ala Lys
80 85 90

aga gaa tta aat ata gtc gct gtt ctg aac tgt atg aac gag ctg ctc			400
Arg Glu Leu Asn Ile Val Ala Val Leu Asn Cys Met Asn Glu Leu Leu			
95	100	105	
gtg ctt cag cgg aag aac ctg ctg gcc cag gag agc gtg gag aca cag			448
Val Leu Gln Arg Lys Asn Leu Leu Ala Gln Glu Ser Val Glu Thr Gln			
110	115	120	
aac ttg aag ctg ggc agt gac atg gac cac ctg cag agc tgc tac gcc			496
Asn Leu Lys Leu Gly Ser Asp Met Asp His Leu Gln Ser Cys Tyr Ala			
125	130	135	
aaa ctt aag gag cag ttg gaa acg tcc agg cgg gag atg atc ggg ctt			544
Lys Leu Lys Glu Gln Leu Glu Thr Ser Arg Arg Glu Met Ile Gly Leu			
140	145	150	155
caa gag aga gac agg cag ctg cag tgc aag aac agg agt ttg cat cag			592
Gln Glu Arg Asp Arg Gln Leu Gln Cys Lys Asn Arg Ser Leu His Gln			
160	165	170	
ctc ctg aat gag aaa gat gag gta caa aaa tta caa aat atc ata			640
Leu Leu Lys Asn Glu Lys Asp Glu Val Gln Lys Leu Gln Asn Ile Ile			
175	180	185	
gcc agc cgg gct act cag tat aat cat gat gtg aag agg aag gag cgt			688
Ala Ser Arg Ala Thr Gln Tyr Asn His Asp Val Lys Arg Lys Glu Arg			
190	195	200	
gaa tat aat aag cta aag gag cgc ctg cat cag ctc gtt atg aac aag			736
Glu Tyr Asn Lys Leu Lys Glu Arg Leu His Gln Leu Val Met Asn Lys			
205	210	215	
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220	225	230	235
gat ggc aaa cga ggc tca tgg agg act gac aaa aca gaa gcc agg aat			832
Asp Gly Lys Arg Gly Ser Trp Arg Thr Asp Lys Thr Glu Ala Arg Asn			
240	245	250	
gaa gat gag atg tac aaa att ctg ttg aat gat tat gag tac cgc cag			880
Glu Asp Glu Met Tyr Lys Ile Leu Leu Asn Asp Tyr Glu Tyr Arg Gln			
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Met Lys Lys Glu Met Ile Ser Leu Leu Ser Pro Gln Lys Lys Lys Pro			
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agg gaa aga gca gag gac ggc aca ggc act gtt gct atc tcc gat ata			1024
Arg Glu Arg Ala Glu Asp Gly Thr Gly Thr Val Ala Ile Ser Asp Ile			
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Cys Asp Thr Val Arg Glu Gln Leu Thr Asn Ser Ile Arg Lys Gln Trp			
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Val His Ser Glu Gly Leu Asn Glu Glu Asp Val Ile Ser Arg Gln Asp			
365	370	375	
cat gag caa gag act gag aaa ctg gag ctg gag att gag cgg tgt aaa			1264
His Glu Gln Glu Thr Glu Lys Leu Glu Leu Glu Ile Glu Arg Cys Lys			
380	385	390	395
gag atg atc aag gct cag cag ctc tta cag cag cag ctg gcc acc			1312
Glu Met Ile Lys Ala Gln Gln Gln Leu Leu Gln Gln Gln Leu Ala Thr			
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acg tgt gat gat gac acc acc tca ctg ttg cga gac tgt tac ttg ctg			1360
Thr Cys Asp Asp Asp Thr Thr Ser Leu Leu Arg Asp Cys Tyr Leu Leu			
415	420	425	
gaa gaa aag gaa cgc ctt aaa gaa gag tgg acc ctt ttt aaa gag caa			1408
Glu Glu Lys Glu Arg Leu Lys Glu Glu Trp Thr Leu Phe Lys Glu Gln			
430	435	440	
aaa aag aat ttt gag aga gaa agg cga agc ttt aca gaa gct gcc att			1456
Lys Lys Asn Phe Glu Arg Glu Arg Arg Ser Phe Thr Glu Ala Ala Ile			
445	450	455	
cga ttg ggg ttg gag aga aag gcg ttt gaa gaa gag cga gcc agc tgg			1504
Arg Leu Gly Leu Glu Arg Lys Ala Phe Glu Glu Glu Arg Ala Ser Trp			
460	465	470	475
gta aag cag cag ttt tta aac atg acg aac ttt gac cac cag aac tca			1552
Val Lys Gln Gln Phe Leu Asn Met Thr Asn Phe Asp His Gln Asn Ser			
480	485	490	
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Glu Asn Val Lys Leu Phe Ser Ala Phe Ser Gly Ser Ser Asp Pro Asp			
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aat ctt ata gtc cac tca cgg cca cgg caa aag aag cta cac agt gtg			1648
Asn Leu Ile Val His Ser Arg Pro Arg Gln Lys Lys Leu His Ser Val			
510	515	520	
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Ala Asn Gly Val Pro Ala Cys Thr Ser Lys Leu Thr Lys Ser Leu Pro			
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20

25

30

Leu Tyr Ser Gln Gln Val Leu Cys Ser Ser Val Pro Leu Ser Lys Asn
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Val His Gly Val Phe Gly Val Phe Cys Thr Gly Glu Asn Ile Glu Gln
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Ser Ile Ser Tyr Leu Asp Gln Glu Leu Thr Thr Phe Gly Phe Pro Ser
65 70 75 80

Leu Tyr Glu Glu Ser Lys Ser Lys Glu Ala Lys Arg Glu Leu Asn Ile
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Val Ala Val Leu Asn Cys Met Asn Glu Leu Leu Val Leu Gln Arg Lys
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Asn Leu Leu Ala Gln Glu Ser Val Glu Thr Gln Asn Leu Lys Leu Gly
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Ser Asp Met Asp His Leu Gln Ser Cys Tyr Ala Lys Leu Lys Glu Gln
130 135 140

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145 150 155 160

Gln Leu Gln Cys Lys Asn Arg Ser Leu His Gln Leu Leu Lys Asn Glu
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Lys Asp Glu Val Gln Lys Leu Gln Asn Ile Ile Ala Ser Arg Ala Thr
180 185 190

Gln Tyr Asn His Asp Val Lys Arg Lys Glu Arg Glu Tyr Asn Lys Leu
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Lys Glu Arg Leu His Gln Leu Val Met Asn Lys Lys Asp Lys Asn Ile
210 215 220

Ala Met Asp Val Leu Asn Tyr Val Gly Arg Ala Asp Gly Lys Arg Gly
225 230 235 240

Ser Trp Arg Thr Asp Lys Thr Glu Ala Arg Asn Glu Asp Glu Met Tyr
245 250 255

Lys Ile Leu Leu Asn Asp Tyr Glu Tyr Arg Gln Lys Gln Ile Leu Met
260 265 270

Glu Asn Ala Glu Leu Lys Val Leu Gln Gln Met Lys Lys Glu Met
275 280 285

Ile Ser Leu Leu Ser Pro Gln Lys Lys Pro Arg Glu Arg Ala Glu
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Asp Gly Thr Gly Thr Val Ala Ile Ser Asp Ile Glu Asp Asp Ser Gly
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Glu Leu Ser Arg Asp Ser Val Trp Gly Leu Ser Cys Asp Thr Val Arg
325 330 335

Glu Gln Leu Thr Asn Ser Ile Arg Lys Gln Trp Arg Ile Leu Lys Ser
340 345 350

His Val Glu Lys Leu Asp Asn Gln Ala Ser Lys Val His Ser Glu Gly
355 360 365

Leu Asn Glu Glu Asp Val Ile Ser Arg Gln Asp His Glu Gln Glu Thr
370 375 380

Glu Lys Leu Glu Leu Glu Ile Glu Arg Cys Lys Glu Met Ile Lys Ala
385 390 395 400

Gln Gln Gln Leu Leu Gln Gln Leu Ala Thr Thr Cys Asp Asp Asp
405 410 415

Thr Thr Ser Leu Leu Arg Asp Cys Tyr Leu Leu Glu Glu Lys Glu Arg
420 425 430

Leu Lys Glu Glu Trp Thr Leu Phe Lys Glu Gln Lys Lys Asn Phe Glu
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Arg Glu Arg Arg Ser Phe Thr Glu Ala Ala Ile Arg Leu Gly Leu Glu
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Phe Ser Ala Phe Ser Gly Ser Ser Asp Pro Asp Asn Leu Ile Val His
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Ser Arg Pro Arg Gln Lys Lys Leu His Ser Val Ala Asn Gly Val Pro
515 520 525

Ala Cys Thr Ser Lys Leu Thr Lys Ser Leu Pro Ala Ser Pro Ser Thr
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Ser Asp Phe Arg Gln Thr His Ser Cys Val Ser Glu His Ser Ser Ile
545 550 555 560

Ser Val Leu Asn Ile Thr Pro Glu Glu Ser Lys Pro Ser Glu Val Ala
565 570 575

Arg Glu Ser Thr Asp Gln Lys Trp Ser Val Gln Ser Arg Pro Ser Ser
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Met Gly Asp Trp Met Thr Val Thr Asp Pro Val

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atg tct ccg tca agt tta tac tcg cag caa gta ctg tgc tct gca aca Met Ser Pro Ser Ser Leu Tyr Ser Gln Gln Val Leu Cys Ser Ala Thr			207
30	35	40	
cct tta tcc aag aat gtg cat ggt gtt ttc agt gcc ttc tgc aca gga Pro Leu Ser Lys Asn Val His Gly Val Phe Ser Ala Phe Cys Thr Gly			255
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60	65	70	75
ttc ggt ttc cct tcc ttg tat gaa gaa tcc aaa agt aag gag gcg aag Phe Gly Phe Pro Ser Leu Tyr Glu Ser Lys Ser Lys Glu Ala Lys			351
80	85	90	
cga gag tta agt ata gtt gct ctt ctg aac tgc atg aat gag ctg ctt Arg Glu Leu Ser Ile Val Ala Leu Leu Asn Cys Met Asn Glu Leu Leu			399
95	100	105	
gtg ctt cag cgg aag aac ctc ctg gcc cag gaa agc gtg gag aca cag Val Leu Gln Arg Lys Asn Leu Leu Ala Gln Glu Ser Val Glu Thr Gln			447
110	115	120	
aat ctg aag ctg ggc agt gac atg gac cac ctg cag agc tgc			